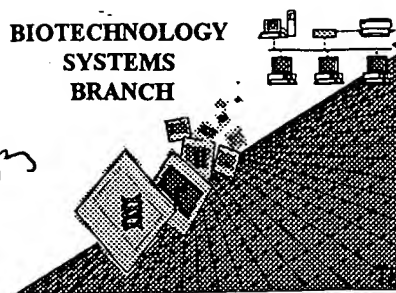


RAW SEQUENCE LISTING
ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH

File logs



#7
RECEIVED

AUG 08 2000

TECH CENTER 1600/2900

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/17/916

Source: 1636

Date Processed by STIC: 7/27/2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

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1636

TECH CENTER 1600/2900

RAW SEQUENCE LISTING DATE: 07/27/2000
 PATENT APPLICATION: US/09/171,916 TIME: 13:43:45

Input Set : A:\NAIR-312 Sequence Listing.txt
 Output Set: N:\CRF3\07272000\I171916.raw

Does Not Comply
 Corrected Diskette Needed

3 <110> APPLICANT: NAIR, SMITA K.
 4 BOCZKOWSKI, DAVID J.
 5 GILBOA, ELI
 7 <120> TITLE OF INVENTION: METHODS FOR TREATING CANCERS AND PATHOGEN INFECTIONS
 8 USING ANTIGEN-PRESENTING CELLS LOADED WITH RNA
 10 <130> FILE REFERENCE: 1579-312
 12 <140> CURRENT APPLICATION NUMBER: 09/171,916
 13 <141> CURRENT FILING DATE: 1999-02-16
 15 <150> PRIOR APPLICATION NUMBER: PCT/US97/07317
 16 <151> PRIOR FILING DATE: 1997-04-30
 18 <150> PRIOR APPLICATION NUMBER: 08/640,444
 19 <151> PRIOR FILING DATE: 1996-04-30
 21 <160> NUMBER OF SEQ ID NOS: 7
 23 <170> SOFTWARE: PatentIn Ver. 2.1
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 4
 27 <212> TYPE: PRT
 28 <213> ORGANISM: Artificial Sequence
 30 <220> FEATURE:
 31 <223> OTHER INFORMATION: Description of Artificial Sequence: Peptide
 33 <400> SEQUENCE: 1
 34 Lys Asp Glu Leu
 35 1
 38 <210> SEQ ID NO: 2
 39 <211> LENGTH: 5
 40 <212> TYPE: PRT
 41 <213> ORGANISM: Artificial Sequence
 43 <220> FEATURE:
 44 <223> OTHER INFORMATION: Description of Artificial Sequence: Peptide
 46 <400> SEQUENCE: 2
 47 Lys Phe Glu Arg Gln
 48 1 5
 51 <210> SEQ ID NO: 3
 52 <211> LENGTH: 4
 53 <212> TYPE: PRT
 54 <213> ORGANISM: Artificial Sequence
 56 <220> FEATURE:
 57 <223> OTHER INFORMATION: Description of Artificial Sequence: Peptide
 59 <400> SEQUENCE: 3
 60 Gln Arg Glu Lys
 61 1
 64 <210> SEQ ID NO: 4
 65 <211> LENGTH: 25
 66 <212> TYPE: PRT
 67 <213> ORGANISM: Artificial Sequence
 69 <220> FEATURE:
 70 <223> OTHER INFORMATION: Description of Artificial Sequence: Peptide

pg 1-2

initial response - see circled portion of
 item 12 on Enon
 summary sheet -
 give source of
 genetic material

RAW SEQUENCE LISTING DATE: 07/27/2000
PATENT APPLICATION: US/09/171,916 TIME: 13:43:45

Input Set : A:\NAIR-312 Sequence Listing.txt
Output Set: N:\CRF3\07272000\I171916.raw

72 <400> SEQUENCE: 4
73 Met Ala Ile Ser Gly Val Pro Val Leu Gly Phe Phe Ile Ile Ala Val
74 1 5 10 15
76 Leu Met Ser Ala Gln Glu Ser Trp Ala
77 20 25
80 <210> SEQ ID NO: 5
81 <211> LENGTH: 24
82 <212> TYPE: DNA
83 <213> ORGANISM: Artificial Sequence
85 <220> FEATURE:
86 <223> OTHER INFORMATION: Description of Artificial Sequence: Probe
88 <400> SEQUENCE: 5
89 cagtttttca aagttgatta tact 24
92 <210> SEQ ID NO: 6
93 <211> LENGTH: 8
94 <212> TYPE: PRT
95 <213> ORGANISM: Artificial Sequence
97 <220> FEATURE:
98 <223> OTHER INFORMATION: Description of Artificial Sequence: Peptide
100 <400> SEQUENCE: 6
101 Ser Ile Ile Asn Phe Glu Lys Leu
102 1 5
105 <210> SEQ ID NO: 7
106 <211> LENGTH: 24
107 <212> TYPE: DNA
108 <213> ORGANISM: Artificial Sequence
110 <220> FEATURE:
111 <223> OTHER INFORMATION: Description of Artificial Sequence: Probe
113 <400> SEQUENCE: 7
114 tcatattagt tgaaactttt tgac 24

VERIFICATION SUMMARY DATE: 07/27/2000
PATENT APPLICATION: US/09/171,916 TIME: 13:43:46

Input Set : A:\NAIR-312 Sequence Listing.txt
Output Set: N:\CRF3\07272000\I171916.raw

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/17/96

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 Skipped Sequences (OLD RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences (NEW RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism (NEW RULES) Sequence(s) are missing this mandatory field or its response.
- 12 Use of <220>Feature (NEW RULES) Sequence(s) are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.